AMENDMENTS TO THE CLAIMS

1. **(Previously Presented)** A method for preparing an array of polynucleotides that is representative of a plurality of first polynucleotides comprising:

a) providing a plurality of samples of double-stranded polynucleotide fragments, wherein each sample is derived from a first polynucleotide;

b) ligating adapters to each end of the polynucleotide fragments of each sample to produce modified polynucleotide fragments, wherein each adapter comprises a first strand and a second strand, the second strand having a region of substantial complementarity to a region of the first strand;

c) using sequences within the adapters to amplify the modified polynucleotide fragments to produce an amplification product for each sample of polynucleotide fragments, wherein each amplification product is representative of the first polynucleotide corresponding to each sample; and

d) applying target solutions comprising the amplification products to one or more substrates, wherein each target solution is applied to a distinct location on one substrate and/or target solutions are applied to different substrates that are combined to produce an array of polynucleotides.

2. **(Canceled)**

3. **(Original)** The method of Claim 1 wherein the double-stranded polynucleotide fragments are derived from a polynucleotide library.

4. **(Original)** The method of Claim 3 wherein the polynucleotide library is a genomic DNA library.

5. **(Original)** The method of Claim 3 wherein the polynucleotide library is a cDNA library.

6. **(Previously Presented)** The method of Claim 3 wherein the double-stranded polynucleotide fragments are derived from YAC, BAC, P1, PAC or cosmid clones.

7. **(Original)** The method of Claim 1 wherein the first polynucleotides each have a complexity of at least about 50 kilobases.

8. **(Original)** The method of Claim 1 wherein the first polynucleotides each have a complexity of at least about 100 kilobases.

9. **(Original)** The method of Claim 7 wherein the first polynucleotides each have a complexity of less than about 500 kilobases.

10. **(Original)** The method of Claim 1 wherein the double-stranded polynucleotide fragments are obtained using one or more restriction endonucleases.

11. **(Original)** The method of Claim 1 wherein the average length of the double-stranded polynucleotide fragments is less than about 5 kilobases.

12. **(Original)** The method of Claim 11 wherein the average length of the double-stranded polynucleotide fragments is less than about 2 kilobases.

13. **(Original)** The method of Claim 11 wherein the average length of the double-stranded polynucleotide fragments is greater than about 100 basepairs.

14. **(Previously Presented)** The method of Claim 1 wherein the average volume of each target solution applied to the substrate is less than about 2 nanoliters.

15. **(Original)** The method of Claim 14 wherein the average volume of each target solution applied to the substrate is equal to greater than about 0.002 nanoliters.

16. **(Previously Presented)** The method of Claim 1 wherein the array comprises at least 1000 amplification products in a 1 cm^2 region of substrate.

17. **(Previously Presented)** The method of Claim 1 wherein the target solutions are robotically spotted on the substrate.

18. **(Previously Presented)** The method of Claim 1 wherein at least one strand of the adapters includes an amino group.

19. **(Original)** The method of Claim 1 wherein the target solutions comprise dimethyl sulfoxide at a concentration of about 20% by volume.

20. **(Previously Presented)** An array of polynucleotides that is representative of a plurality of first polynucleotides wherein said array is produced according to the method of Claim 1 and comprises at least 1000 amplification products in a 1 cm^2 region of substrate.

21. **(Previously Presented)** A plurality of target solutions useful for forming an array of polynucleotides that is representative of a plurality of first polynucleotides, wherein said target solutions are prepared by a method comprising:

a) providing a plurality of samples of double-stranded polynucleotide fragments, wherein each sample is derived from a first polynucleotide;

b) ligating adapters to each end of the polynucleotide fragments of each sample to produce modified polynucleotide fragments, wherein each adapter comprises a first strand and a second strand, the second strand having a region of substantial complementarity to a region of the first strand;

c) using sequences within the adapters to amplify the modified polynucleotide fragments to produce an amplification product for each sample of polynucleotide fragments, wherein each amplification product is representative of the first polynucleotide corresponding to each sample; and

d) forming target solutions from the amplification products, wherein the target solutions comprise dimethyl sulfoxide at a concentration of about 20% by volume and are suitable for application to a substrate to produce an array of polynucleotides

wherein:

the double-stranded polynucleotide fragments are derived from a polynucleotide library.

22. **(Canceled)**

23. **(Previously Presented)** The method of Claim 1 wherein each amplification product for each sample is isolated and resuspended to form the target solution for that sample.

24. **(Previously Presented)** The plurality of target solutions of Claim 21 wherein each amplification product for each sample is isolated and resuspended to form the target solution for that sample.

25. **(Previously Presented)** The method of Claim 1 wherein the first polynucleotides each have a complexity of at least about 20 kilobases.